



SEQUENCE LISTING

<110> Potter, Robert  
Rosenthal, Kim

<120> High Fidelity Reverse Transcriptases and Uses Thereof

<130> 0942.5030001/RWE/HCC

<140> 09/808,124

<141> 2001-03-15

<150> 60/189,454

<151> 2000-03-15

<160> 6

<170> PatentIn version 3.0

<210> 1

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide template

<400> 1

gagttacagt gtttttggtc cagtctgtag cagtgtgtga atggaag

47

<210> 2

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide primer

<400> 2

cttcattca cacactgc

18

<210> 3

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide primer

<400> 3

gaagatcgca ctccagccag c

21

<210> 4

<211> 298

<212> DNA

<213> Artificial Sequence

<220>

<223> lacZa peptide in M13mp19 from SuperScript II RT and  
SuperScript II H203R T306K F309N

<400> 4

agcgcaacgc aattaatgtg agttagctca ctccattaggc accccaggct ttacacttta 60

tgcttccggc tcgtatgttg tgtggaattg tgagcggata acaatttcac acaggaaaca 120

gctatgacca tgattacgcc aagcttgcac gctgcaggt cgactctaga ggatccccgg 180

gtaccgagct cgaattcact ggccgtcggt ttacaacgtc gtgactggga aaaccctggc 240  
 gttacccaac ttaatcgct tgcagcacat ccccttttcg ccagctggcg taatagcg 298

<210> 5

<211> 1515

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1)..(1515)

<400> 5

atg acc cta aat ata gaa gat gag cat cgg cta cat gag acc tca aaa	48
Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys	
1 5 10 15	
gag cca gat gtt tct cta ggg tcc aca tgg ctg tct gat ttt cct cag	96
Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln	
20 25 30	
gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct	144
Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro	
35 40 45	
ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa	192
Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln	
50 55 60	
tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag	240
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln	
65 70 75 80	
aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac	288
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn	
85 90 95	
acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct	336
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro	
100 105 110	
gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc	384
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro	
115 120 125	
acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc cca ccg tcc cac	432

Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Pro	Pro	Ser	His	
130						135					140					
cag	tgg	tac	act	gtg	ctt	gat	tta	aag	gat	gcc	ttt	ttc	tgc	ctg	aga	480
Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe	Phe	Cys	Leu	Arg	
145					150					155					160	
ctc	cac	ccc	acc	agt	cag	cct	ctc	ttc	gcc	ttt	gag	tgg	aga	gat	cca	528
Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	Trp	Arg	Asp	Pro	
				165					170					175		
gag	atg	gga	atc	tca	gga	caa	ttg	acc	tgg	acc	aga	ctc	cca	cag	ggg	576
Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg	Leu	Pro	Gln	Gly	
			180				185						190			
ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	cac	aga	gac	cta	624
Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	His	Arg	Asp	Leu	
		195					200					205				
gca	gac	ttc	cgg	atc	cag	cac	cca	gac	ttg	atc	ctg	cta	cag	tac	gtg	672
Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu	Leu	Gln	Tyr	Val	
	210					215					220					
gat	gac	tta	ctg	ctg	gcc	gcc	act	tct	gag	cta	gac	tgc	caa	caa	ggg	720
Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp	Cys	Gln	Gln	Gly	
225					230					235					240	
act	cgg	gcc	ctg	tta	caa	acc	cta	ggg	aac	ctc	ggg	tat	cgg	gcc	tcg	768
Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly	Tyr	Arg	Ala	Ser	
				245					250					255		
gcc	aag	aaa	gcc	caa	att	tgc	cag	aaa	cag	gtc	aag	tat	ctg	ggg	tat	816
Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys	Tyr	Leu	Gly	Tyr	
			260					265					270			
ctt	cta	aaa	gag	ggg	cag	aga	tgg	ctg	act	gag	gcc	aga	aaa	gag	act	864
Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala	Arg	Lys	Glu	Thr	
		275					280					285				
gtg	atg	ggg	cag	cct	act	ccg	aag	acc	cct	cga	caa	cta	agg	gag	ttc	912
Val	Met	Gly	Gln	Pro	Thr	Pro	Lys	Thr	Pro	Arg	Gln	Leu	Arg	Glu	Phe	
	290					295					300					
cta	ggg	acg	gca	ggc	ttc	tgt	cgc	ctc	tgg	atc	cct	ggg	ttt	gca	gaa	960
Leu	Gly	Thr	Ala	Gly	Phe	Cys	Arg	Leu	Trp	Ile	Pro	Gly	Phe	Ala	Glu	
305					310					315					320	
atg	gca	gcc	ccc	ttg	tac	cct	ctc	acc	aaa	acg	ggg	act	ctg	ttt	aat	1008
Met	Ala	Ala	Pro	Leu	Tyr	Pro	Leu	Thr	Lys	Thr	Gly	Thr	Leu	Phe	Asn	
				325					330					335		
tgg	ggc	cca	gac	caa	caa	aag	gcc	tat	caa	gaa	atc	aag	caa	gct	ctt	1056
Trp	Gly	Pro	Asp	Gln	Gln	Lys	Ala	Tyr	Gln	Glu	Ile	Lys	Gln	Ala	Leu	
			340					345					350			
cta	act	gcc	cca	gcc	ctg	ggg	ttg	cca	gat	ttg	act	aag	ccc	ttt	gaa	1104
Leu	Thr	Ala	Pro	Ala	Leu	Gly	Leu	Pro	Asp	Leu	Thr	Lys	Pro	Phe	Glu	

355	360	365	
ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln 370 375 380			1152
aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu 385 390 395 400			1200
gac cca gta gca gct ggg tgg ccc cct tgc cta cgg atg gta gca gcc Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala 405 410 415			1248
att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro 420 425 430			1296
cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro 435 440 445			1344
ccc gac cgc tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu 450 455 460			1392
ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn 465 470 475 480			1440
ccg gct acg ctg ctc cca ctg cct gag gaa ggg ctg caa cac aac tgc Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys 485 490 495			1488
ctt gat aat tcc cgc tta att aat taa Leu Asp Asn Ser Arg Leu Ile Asn 500			1515

<210> 6

<211> 504

<212> PRT

<213> Moloney Murine Leukemia Virus

<400> 6

Met Thr Leu Asn Ile Glu Asp Glu His Arg Leu His Glu Thr Ser Lys
1 5 10 15

Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln
20 25 30

Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro  
 35 40 45

Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln  
 50 55 60

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln  
 65 70 75 80

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn  
 85 90 95

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro  
 100 105 110

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro  
 115 120 125

Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His  
 130 135 140

Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg  
 145 150 155 160

Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro  
 165 170 175

Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly  
 180 185 190

Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu His Arg Asp Leu  
 195 200 205

Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val  
 210 215 220

Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly  
 225 230 235 240

Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly Tyr Arg Ala Ser  
 245 250 255

Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr  
 260 265 270

Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr  
 275 280 285

Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe  
 290 295 300

Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu  
 305 310 315 320

Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn  
 325 330 335

Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu  
 340 345 350

Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu  
 355 360 365

Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln  
 370 375 380

Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu  
 385 390 395 400

Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala  
 405 410 415

Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro  
 420 425 430

Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro  
 435 440 445

Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu  
 450 455 460

Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn  
 465 470 475 480

Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys

485

490

495

Leu Asp Asn Ser Arg Leu Ile Asn  
...500.